UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Offic
Addr ss: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

VB

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
09/147,405	04/01/98	GUSS B	REF/GUSS/P33

HM12/1206

BACON & THOMAS
625 SLATERS LANE 4TH FLOOR
ALEXANDRIA VA 22314-1176

EXAMINER	
LEE, L	
ART UNIT	**PAPER NUMBER**
1645	9

DATE MAILED: 12/06/99

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

DETAILED ACTION

Nucleotide and /or Amino acid Sequence Disclosures

1. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. See the attached Raw Sequence Listing Error Report. Applicants are reminded that all the sequences disclosed in the application need to be comply with the requirements. It is noted that the sequences in the claims and figures in this application fail to comply with the requirements of 37 CFR 1.821 through 1.825.

APPLICANT IS GIVEN A ONE MONTH EXTENDABLE PERIOD WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Election/Restrictions

2. Restriction is required under 35 U.S.C. 121 and 372.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In accordance with 37 CFR 1.499, applicant is required, in response to this action, to elect a single invention to which the claims must be restricted.

Group I, claim(s) 1 and 25, drawn to a protein or polypeptide.

Group II, claim(s) 2-11 and 26, drawn to recombinant DNA molecule, expression system, and method for producing the protein.

Group III, claim(s) 12-14, drawn to the use of a protein from staphylococci to block the adherence of staphylococci to surfaces with immobilized fibrinogen.

Group IV, claim(s) 15, drawn to the use of a protein from staphylococci to isolate fibrinogen.

Group V, claim(s) 16, drawn to the use of a gene to detect the presence of *S. epidermidis*.

Group VI, claim(s) 17, drawn to antibodies.

Group VII, claim(s) 18, drawn to the use of antibodies for diagnostic purpose.

Group VIII, claim(s) 19 and 29, drawn to the use of antibodies for therapeutic purposes.

Group IX, claim(s) 20-22, drawn to the use of antibodies to block the adherence of Staphylococci.

Group X, claim(s) 23-24 and 27, drawn to the use a protein from Staphylococci as an immunogen.

Group XI, claim(s) 28, drawn to a method of active immunization administering the DNA sequence.

3. The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The inventions listed as Groups I-XI do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The technical feature linking groups I-XI appears to be that they relate to a polypeptide designated as a protein or a polypeptide having fibrinogen binding activity from a coagulase-negative staphylococci strain.

However, Heimburger et al (US 4,245,039, Jan 13, 1991) teach a protein (clumping factor) having fibrinogen binding activity from a coagulase-negative staphylococci strain, staphylococcus aureus Newman D2C (column 2, lines 18-26).

Therefore, the technical feature linking the inventions of groups I-XI does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art.

The special technical feature of Group I is considered to be a a protein or polypeptide or a vaccine composition characterized as the protein having fibrinogen binding activity from a coagulase-negative staphylococci strain.

The special technical feature of Group II is considered to be a recombinant DNA molecule, expression system, and method for producing the protein.

The special technical feature of Group III is considered to be the use of a protein from staphylococci to block the adherence of staphylococci to surfaces with immobilized fibrinogen.

The special technical feature of Group IV is considered to be the use of a protein from staphylococci to isolate fibrinogen.

The special technical feature of Group V is considered to be the use of a gene to detect the presence of *S. epidermidis*.

The special technical feature of Group VI is considered to be antibodies raised against the protein.

The special technical feature of Group VII is considered to be the use of antibodies for diagnostic purpose.

The special technical feature of Group VIII is considered to be the use of antibodies for therapeutic purposes.

The special technical feature of Group IX is considered to be the use of antibodies to block the adherence of Staphylococci.

The special technical feature of Group X is considered to be the use a protein from Staphylococci as an immunogen.

The special technical feature of Group XI is considered to be a method of active immunization administering the DNA sequence.

4. Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a petition under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(I).

Any inquiry of a general nature or relating to the status of this general application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Papers relating to this application may be submitted to Technology Center 1600, Group 1645 by facsimile transmission. The faxing of such papers must conform with the notice published in the Official Gazette, 1096 OG 30 (November 15, 1989). Should applicant wish to FAX a response, the current FAX number for Group 1600 is (703) 308-4242.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Li Lee, M.D., Ph.D. whose telephone number is (703) 308-8891. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached at (703) 308-3995.

Li Lee, M.D., Ph.D.
November 24, 1999

ANTHONY C. CAPUTA
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/147,405

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Us of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source f genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please d not use "C py to Disk" function of PatentIn versi n 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

Li Lee

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/147,405

DATE: 11/15/1999
TIME: 10:51:16

Input Set: I147405.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: Guss, Bengt
Nilsson, Martin
Frykberg, Lars
Flock, Jan-Ingmar
Lindberg, Martin
<120> TITLE OF INVENTION: Fibrinogen Binding Protein Originating from Coagulase-Negative Staphylococcus
<130> FILE REFERENCE: guss 09/147405
<140> CURRENT APPLICATION NUMBER: US/09/147,405
<141> CURRENT FILING DATE: 1998-04-01
<150> EARLIER APPLICATION NUMBER: PCT/SE97/10191
<151> EARLIER FILING DATE: 1997-06-18
<150> EARLIER APPLICATION NUMBER: SE 9602496-3
<151> EARLIER FILING DATE: 1996-06-20
<160> NUMBER OF SEQ ID NOS: 15
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO 1
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 1
caacaaccat ctcacacaac 20
<210> SEQ ID NO 2
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 2
catcaaattg atatttccca tc 22
<210> SEQ ID NO 3
<211> LENGTH: 18
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis
<400> SEQUENCE: 3
W--> gantcngant cngcnagn 18
0 0 0 0 see item 10 on Error Summary Sheet
<210> SEQ ID NO 4
<211> LENGTH: 19
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer

<400> SEQUENCE: 4
aggtcaagga caaggtgac 19
<210> SEQ ID NO 5
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 5
ccgatgaaaa tggaaagtat c 21
<210> SEQ ID NO 6
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 6
tccgttatct atactaaagt c 21
<210> SEQ ID NO 7
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 7
actgatcatg atgactttag t 21
<210> SEQ ID NO 8
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 8
gcggatccaa tcagtcaata aacaccgacg at 32
<210> SEQ ID NO 9
<211> LENGTH: 32
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
<400> SEQUENCE: 9
cggaattctg ttcggactga tttggaagtt cc 32
<210> SEQ ID NO 10
<211> LENGTH: 1781
<212> TYPE: DNA
<213> ORGANISM: Staphylococcus epidermidis
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (3)..(1781)
<400> SEQUENCE: 10

```
ac cac cac cac cac cac cac ccc tct agt gat gaa gaa aag aat gat    47
   His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp
     1               5                  10                  15
gtg atc aat aat aat cag tca ata aac acc gac gat aat aac caa ata   95
Val Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile
                20                  25                  30
att aaa aaa gaa gaa acg aat aac tac gat ggc ata gaa aaa cgc tca   143
Ile Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser
            35                  40                  45
gaa gat aga aca gag tca aca aca aat gta gat gaa aac gaa gca aca   191
Glu Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr
        50                  55                  60
ttt tta caa aag acc cct caa gat aat act cat ctt aca gaa gaa gag   239
Phe Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu
    65                  70                  75
gta aaa gaa tcc tca tca gtc gaa tcc tca aat tca tca att gat act   287
Val Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr
80                  85                  90                  95
gcc caa caa cca tct cac aca aca ata aat aga gaa gaa tct gtt caa   335
Ala Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln
                100                 105                 110
aca agt gat aat gta gaa gat tca cac gta tca gat ttt gct aac tct   383
Thr Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser
            115                 120                 125
aaa ata aaa gag agt aac act gaa tct ggt aaa gaa gag aat act ata   431
Lys Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile
        130                 135                 140
gag caa cct aat aaa gta aaa gaa gat tca aca aca agt cag ccg tct   479
Glu Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser
    145                 150                 155
ggc tat aca aat ata gat gaa aaa att tca aat caa gat gag tta tta   527
Gly Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu
160                 165                 170                 175
aat tta cca ata aat gaa tat gaa aat aag gct aga cca tta tct aca   575
Asn Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr
                180                 185                 190
aca tct gcc caa cca tcg att aaa cgt gta acc gta aat caa tta gcg   623
Thr Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala
            195                 200                 205
gcg gaa caa ggt tcg aat gtt aac cat tta att aaa gtt act gat caa   671
Ala Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln
        210                 215                 220
agt att act gaa gga tat gat gat agt gaa ggt gtt att aaa gca cat   719
Ser Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His
    225                 230                 235
gat gct gaa aac tta atc tat gat gta act ttt gaa gta gat gat aag   767
Asp Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys
240                 245                 250                 255
gtg aaa tct ggt gat acg atg aca gtg gat ata gat aag aat aca gtt   815
Val Lys Ser Gly Asp Thr Met Thr Val Asp Ile Asp Lys Asn Thr Val
```

```
                    260                 265                 270
cca tca gat tta acc gat agc ttt aca ata cca aaa ata aaa gat aat   863
Pro Ser Asp Leu Thr Asp Ser Phe Thr Ile Pro Lys Ile Lys Asp Asn
                275                 280                 285
tct gga gaa atc atc gct aca ggt act tat gat aac aaa aat aaa caa   911
Ser Gly Glu Ile Ile Ala Thr Gly Thr Tyr Asp Asn Lys Asn Lys Gln
        290                 295                 300
atc acc tat act ttt aca gat tat gta gat aag tat gaa aat att aaa   959
Ile Thr Tyr Thr Phe Thr Asp Tyr Val Asp Lys Tyr Glu Asn Ile Lys
    305                 310                 315
gca cac ctt aaa tta acg tca tac att gat aaa tca aag gtt cca aat   1007
Ala His Leu Lys Leu Thr Ser Tyr Ile Asp Lys Ser Lys Val Pro Asn
320                 325                 330                 335
aat aat acc aag tta gat gta gaa tat aaa acg gcc ctt tca tca gta   1055
Asn Asn Thr Lys Leu Asp Val Glu Tyr Lys Thr Ala Leu Ser Ser Val
                340                 345                 350
aat aaa aca att acg gtt gaa tat caa aga cct aac gaa aat cgg act   1103
Asn Lys Thr Ile Thr Val Glu Tyr Gln Arg Pro Asn Glu Asn Arg Thr
            355                 360                 365
gct aac ctt caa agt atg ttt aca aat ata gat acg aaa aat cat aca   1151
Ala Asn Leu Gln Ser Met Phe Thr Asn Ile Asp Thr Lys Asn His Thr
        370                 375                 380
gtt gag caa acg att tat att aac cct ctt cgt tat tca gcc aag gaa   1199
Val Glu Gln Thr Ile Tyr Ile Asn Pro Leu Arg Tyr Ser Ala Lys Glu
    385                 390                 395
aca aat gta aat att tca ggg aat ggt gat gaa ggt tca aca att ata   1247
Thr Asn Val Asn Ile Ser Gly Asn Gly Asp Glu Gly Ser Thr Ile Ile
400                 405                 410                 415
gac gat agc aca ata att aaa gtt tat aag gtt gga gat aat caa aat   1295
Asp Asp Ser Thr Ile Ile Lys Val Tyr Lys Val Gly Asp Asn Gln Asn
                420                 425                 430
tta cca gat agt aac aga att tat gat tac agt gaa tat gaa gat gtc   1343
Leu Pro Asp Ser Asn Arg Ile Tyr Asp Tyr Ser Glu Tyr Glu Asp Val
            435                 440                 445
aca aat gat gat tat gcc caa tta gga aat aat aat gat gtg aat att   1391
Thr Asn Asp Asp Tyr Ala Gln Leu Gly Asn Asn Asn Asp Val Asn Ile
        450                 455                 460
aat ttt ggt aat ata gat tca cca tat att att aaa gtt att agt aaa   1439
Asn Phe Gly Asn Ile Asp Ser Pro Tyr Ile Ile Lys Val Ile Ser Lys
    465                 470                 475
tat gac cct aat aag gat gat tac acg act ata cag caa act gtg aca   1487
Tyr Asp Pro Asn Lys Asp Asp Tyr Thr Thr Ile Gln Gln Thr Val Thr
480                 485                 490                 495
atg cag acg act ata aat gag tat act ggt gag ttt aga aca gca tcc   1535
Met Gln Thr Thr Ile Asn Glu Tyr Thr Gly Glu Phe Arg Thr Ala Ser
                500                 505                 510
tat gat aat aca att gct ttc tct aca agt tca ggt caa gga caa ggt   1583
Tyr Asp Asn Thr Ile Ala Phe Ser Thr Ser Ser Gly Gln Gly Gln Gly
            515                 520                 525
gac ttg cct cct gaa aaa act tat aaa atc gga gat tac gta tgg gaa   1631
```

```
195         Asp Leu Pro Pro Glu Lys Thr Tyr Lys Ile Gly Asp Tyr Val Trp Glu
196                 530                 535                 540
197         gat gta gat aaa gat ggt att caa aat aca aat gat aat gaa aaa ccg   1679
198         Asp Val Asp Lys Asp Gly Ile Gln Asn Thr Asn Asp Asn Glu Lys Pro
199             545                 550                 555
200         ctt agt aat gta ttg gta act ttg acg tat cct gat gga act tca aaa   1727
201         Leu Ser Asn Val Leu Val Thr Leu Thr Tyr Pro Asp Gly Thr Ser Lys
202         560                 565                 570                 575
203         tca gtc aga aca gat gaa gat ggg aaa tat caa ttt gat ggg gtg cag   1775
204         Ser Val Arg Thr Asp Glu Asp Gly Lys Tyr Gln Phe Asp Gly Val Gln
205                         580                 585                 590
206         gtc gac                                                       1781
207         Val Asp
208     <210> SEQ ID NO 11
209     <211> LENGTH: 593
210     <212> TYPE: PRT
211     <213> ORGANISM: Staphylococcus epidermidis
212     <400> SEQUENCE: 11
213         His His His His His His Pro Ser Ser Asp Glu Glu Lys Asn Asp Val
214           1               5                  10                  15
215         Ile Asn Asn Asn Gln Ser Ile Asn Thr Asp Asp Asn Asn Gln Ile Ile
216                      20                  25                  30
217         Lys Lys Glu Glu Thr Asn Asn Tyr Asp Gly Ile Glu Lys Arg Ser Glu
218                  35                  40                  45
219         Asp Arg Thr Glu Ser Thr Thr Asn Val Asp Glu Asn Glu Ala Thr Phe
220              50                  55                  60
221         Leu Gln Lys Thr Pro Gln Asp Asn Thr His Leu Thr Glu Glu Glu Val
222          65                  70                  75                  80
223         Lys Glu Ser Ser Ser Val Glu Ser Ser Asn Ser Ser Ile Asp Thr Ala
224                          85                  90                  95
225         Gln Gln Pro Ser His Thr Thr Ile Asn Arg Glu Glu Ser Val Gln Thr
226                     100                 105                 110
227         Ser Asp Asn Val Glu Asp Ser His Val Ser Asp Phe Ala Asn Ser Lys
228                 115                 120                 125
229         Ile Lys Glu Ser Asn Thr Glu Ser Gly Lys Glu Glu Asn Thr Ile Glu
230             130                 135                 140
231         Gln Pro Asn Lys Val Lys Glu Asp Ser Thr Thr Ser Gln Pro Ser Gly
232         145                 150                 155                 160
233         Tyr Thr Asn Ile Asp Glu Lys Ile Ser Asn Gln Asp Glu Leu Leu Asn
234                         165                 170                 175
235         Leu Pro Ile Asn Glu Tyr Glu Asn Lys Ala Arg Pro Leu Ser Thr Thr
236                     180                 185                 190
237         Ser Ala Gln Pro Ser Ile Lys Arg Val Thr Val Asn Gln Leu Ala Ala
238                 195                 200                 205
239         Glu Gln Gly Ser Asn Val Asn His Leu Ile Lys Val Thr Asp Gln Ser
240             210                 215                 220
241         Ile Thr Glu Gly Tyr Asp Asp Ser Glu Gly Val Ile Lys Ala His Asp
242         225                 230                 235                 240
243         Ala Glu Asn Leu Ile Tyr Asp Val Thr Phe Glu Val Asp Asp Lys Val
244                         245                 250                 255
```

VERIFICATION SUMMARY
PATENT APPLICATION US/09/147,405

DATE: 11/15/1999
TIME: 10:51:16

Input Set: I147405.RAW

Line	?	Error/Warning	Original Text
38	W	"N" or "Xaa" used: Feature required	gantcngant cnganagn

Application No.: 09/147,405

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An ~~initial or~~ substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An ~~initial or~~ substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE